

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: March 24, 2003, 15:46:23 ; Search time 9.41818 Seconds

(without alignments)
1225.145 Million cell updates/sec

Title: US-09-988-971-2_COPY_35_90
Perfect score: 288
Sequence: 1 ATVALGSEFPAGPAELSLR.....VLSEVSGREYNIPSHVAKV 56

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: SP_ARCHAEA:*
2: SP_BACTERIA:*
3: SP_FUNGI:*
4: SP_HUMAN:*
5: SP_INVERTEBRATE:*
6: SP_MAMMAL:*
7: SP_MHC:*
8: SP_ORGANELLE:*
9: SP_PHAGE:*
10: SP_PLANT:*
11: SP_RODENT:*
12: SP_VIRUS:*
13: SP_VERTEBRATE:*
14: SP_UNCLASSIFIED:*
15: SP_VIRUS:*
16: SP_BACTERIAP:*
17: SP_ARCHAEP:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	288	100.0	210 4 O8WY18	O8WY18 homo sapien
2	288	100.0	261 4 O8H6Q3	O8H6Q3 homo sapien
3	242	84.0	259 11 O8V142	O8V142 mus musculu
4	242	84.0	259 11 O8R4L0	O8R4L0 mus musculu
5	143	49.7	197 4 O9H135	O9H135 homo sapien
6	140	48.6	63 4 O96Q14	O96Q14 homo sapien
7	109.5	38.0	517 5 O77050	O77050 anthocidaxi
8	100	34.7	505 4 O96IN1	O96IN1 homo sapien
9	99	34.4	161 4 O9HBI7	O9HBI7 homo sapien
10	99	34.4	216 4 O13239	O13239 homo sapien
11	97	33.7	280 11 O8QZX8	O8QZX8 mus musculu
12	97	33.7	281 11 O60898	O60898 mus musculu
13	95.5	33.2	527 5 O9Y121	O9Y121 ephydactia f
14	93	32.3	511 5 O8MQM5	O8MQM5 strongyloce
15	91.5	31.8	517 5 O9V9J3	O9V9J3 drosophila
16	90	31.2	121 4 O9H4Y2	O9H4Y2 homo sapien

17	90	31.2	502 13 O9DDK6	O9DDK6 salmo salar
18	88	30.6	509 6 O95M32	O95M32 hylobates s
19	88	30.6	509 11 O91X65	O91X65 mus musculu
20	87.5	30.4	153 13 O91878	O91878 brachydanio
21	87.5	30.4	193 13 O90993	O90993 gallus gall
22	87.5	30.4	204 15 O85730	O85730 rous sarcom
23	87.5	30.4	285 15 O85476	O85476 rous sarcom
24	87.5	30.4	526 15 O60567	O60567 rous sarcom
25	87.5	30.4	526 15 O92806	O92806 rous sarcom
26	87.5	30.4	587 15 O64817	O64817 avian sarco
27	87	30.2	488 13 O13064	O13064 xenopus lae
28	87	30.2	509 6 O95K87	O95K87 saimiri scl
29	85	29.5	1049 5 O00851	O00851 entamoeba h
30	84.5	29.3	495 5 O8MSU4	O8MSU4 ephydactia f
31	84.5	29.3	541 11 O99PW1	O99PW1 rattus norv
32	83.5	29.0	527 13 O91552	O91552 xiphophorus
33	83.5	29.0	534 4 O16248	O16248 homo sapien
34	83.5	29.0	534 6 O95M31	O95M31 hylobates s
35	82.5	28.6	537 11 O62844	O62844 rattus norv
36	82.5	28.6	504 5 O8MSU2	O8MSU2 ephydactia f
37	82.5	28.6	542 11 O9J110	O9J110 rattus norv
38	82.5	28.6	682 5 O25432	O25432 lyrechinus
39	82	28.5	496 13 O93411	O93411 xenopus lae
40	81.5	28.3	523 15 O85477	O85477 rous sarcom
41	81.5	28.3	526 15 O64993	O64993 rous sarcom
42	81.5	28.3	526 15 O64994	O64994 rous sarcom
43	81.5	28.3	526 15 O93080	O93080 rous sarcom
44	81.5	28.3	535 15 O92957	O92957 rous sarcom
45	81.5	28.3	545 15 O86362	O86362 rous sarcom

ALIGNMENTS

RESULT 1
O8WY18 PRELIMINARY; PRT; 210 AA.
AC O8WY18;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Modulator of antigen receptor signaling, putative splice isoform
DE WARS-V.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
CX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=THYMUS;
RA Loreto M.P., Meglade C.J.;
RT "Modulator of Antigen Receptor Signaling (WARS) - putative splice variant.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF290986; AAL38198.1; -
DR InterPro: IPR000980; SH2.
DR InterPro: IPR001452; SH3.
DR Pfam: PF00017; SH2; 1.
DR Pfam: PF00018; SH3; 1.
DR PRINTS: PR00401; SH2DOMAIN.
DR PRINTS: PR00452; SH3DOMAIN.
DR PRODOM: PD000093; SH2; 1.
DR SMART: SM00252; SH2; 1.
DR SMART: SM00326; SH3; 1.
DR PROSITE: PSS0001; SH2; 1.
DR PROSITE: PSS0002; SH3; 1.
KW RECEPTOR.
SQ SEQUENCE 210 AA; 23103 MW; BED62208E53A472E CRC64;
Query Match 100.0%; Score 288; DB 4; Length 210;
Best Local Similarity 100.0%; Pred. No. 4.5e-27;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATVALGSPAGGPAELSLRLGEPITVSDGDWMTVLSVSGREYNIPSVYAKV 56
 DB 35 ATVALGSPAGGPAELSLRLGEPITVSDGDWMTVLSVSGREYNIPSVYAKV 90

RESULT 2
 ID Q9H6Q3 PRELIMINARY; PRT; 261 AA.

AC Q9H6Q3;
 DT 01-MAR-2001 (TRENBLrel. 16, Created)
 DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
 DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
 DE CDNA: FL211992 f18, clone HEP06554 (Src-like adapter protein-2)
 DE (Modulator of antigen receptor signaling MARS).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 NCBI_Taxid=9606;
 [1]
 RN SEQUENCE FROM N.A.
 RA Kawabata A., Hiki J., Kobayashi N., Inagaki H., Ikema Y., Okamoto S.,
 RA Okitani R., Ota T., Suzuki Y., Ohsashi M., Nishi T., Shibahara T.,
 RA Tanaka T., Nakamura Y., Isogai T., Sugano S.;
 RT "NEBO human cDNA sequencing project."
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
 [2]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=21553259; PubMed=11696592;
 RA Holland S.J., Liao X.C., Mendenhall M.K., Zhou X., Pardo J., Chu P.,
 RA Spencer C., Fu A.C., Sheng N., Yu P., Pal E., Negin A., Shen M.,
 RA Yu S., Chan E., Wu X., Li C., Weisenschlager M., Averis G.,
 RA Kolbinger F., Bennett M.K., Molineux S., Luo Y., Payan D.G.,
 RA Manobo H.S.Y., Wu J.;
 RT "Functional Cloning of Src-like Adapter Protein-2 (SLAP-2), a Novel
 RT Inhibitor of Antigen Receptor Signaling."
 RL J. Exp. Med. 194:1263-1276(2001).
 [3]
 RN [3]
 RP SEQUENCE FROM N.A.
 RA TISSUE=THYMUS;
 RC Loreto M.P., McGlade C.J.;
 RT "Modulator of Antigen Receptor Signaling (MARS)."
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
 DR EMBL: AK025645; BAB15201.1; -;
 DR EMBL: AF363553; AAL29204.1; -;
 DR EMBL: AF20985; AAL38197.1; -;
 DR HSPB; P06239; ILK.
 DR InterPro; IPR000980; SH2.
 DR InterPro; IPR001452; SH3.
 DR Pfam; PF00017; SH2; 1.
 DR Pfam; PF00018; SH3; 1.
 DR PRINTS; PR00401; SH2DOMAIN.
 DR ProDom; PD000093; SH2; 1.
 DR SMART; SM00252; SH2; 1.
 DR SMART; SM00326; SH3; 1.
 DR PROSITE; PS50001; SH2; 1.
 DR PROSITE; PS50002; SH3; 1.
 KW SH3 domain; Receptor.
 SQ SEQUENCE 261 AA; 28585 MW; 858AF03451672B3D CRC64;

Query Match 100.0%; Score 288; DB 4; Length 261;
 Best Local Similarity 100.0%; Pred. No. 5, 8e-27;
 Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATVALGSPAGGPAELSLRLGEPITVSDGDWMTVLSVSGREYNIPSVYAKV 56
 DB 35 ATVALGSPAGGPAELSLRLGEPITVSDGDWMTVLSVSGREYNIPSVYAKV 90

RESULT 3
 ID Q8VI42 PRELIMINARY; PRT; 259 AA.
 AC Q8VI42;

DT 01-MAR-2002 (TRENBLrel. 20, Created)
 DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)
 DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
 DE Modulator of antigen receptor signaling MARS.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_Taxid=10090;
 [1]
 RN SEQUENCE FROM N.A.
 RA Loreto M.P., McGlade C.J.;
 RT "Modulator of Antigen Receptor Signaling (MARS)."
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF287457; AAL38196.1; -;
 DR InterPro; IPR000980; SH2.
 DR InterPro; IPR001452; SH3.
 DR Pfam; PF00017; SH2; 1.
 DR Pfam; PF00018; SH3; 1.
 DR PRINTS; PR00401; SH2DOMAIN.
 DR ProDom; PD000093; SH2; 1.
 DR SMART; SM00252; SH2; 1.
 DR SMART; SM00326; SH3; 1.
 DR PROSITE; PS50001; SH2; 1.
 DR PROSITE; PS50002; SH3; 1.
 KW Receptor.
 SQ SEQUENCE 259 AA; 28476 MW; 8270F17CD3FC50A3 CRC64;

Query Match 84.0%; Score 242; DB 11; Length 259;
 Best Local Similarity 85.5%; Pred. No. 2, 2e-21;
 Matches 47; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 2 TAVALGSPAGGPAELSLRLGEPITVSDGDWMTVLSVSGREYNIPSVYAKV 56
 DB 35 TAVALGSPAGGPAELSLRLGEPITVSDGDWMTVLSVSGREYNIPSVYAKV 89

RESULT 4
 ID Q8R4L0 PRELIMINARY; PRT; 259 AA.

AC Q8R4L0;
 DT 01-JUN-2002 (TRENBLrel. 21, Created)
 DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
 DE Src-like adapter protein-2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_Taxid=10090;
 [1]
 RN SEQUENCE FROM N.A.
 RA Pandey A., Ibarrol N., Kratchmarova I., Fernandez M.,
 RA Constantinescu S., Ohara O., Sawadkowsky S., Lodish H.F., Mann M.;
 RT "A novel Src homology 2 domain-containing molecule, Src-like Adapter
 RT Protein-2 (SLAP-2), which negatively regulates T cell receptor
 RT signaling."
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 [2]
 RN SEQUENCE FROM N.A.
 RA Ibarrola N., Mann M., Pandey A.;
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF434990; AAL66403.1; -;
 SQ SEQUENCE 259 AA; 28516 MW; 1388E6824152E34 CRC64;

Query Match 84.0%; Score 242; DB 11; Length 259;
 Best Local Similarity 85.5%; Pred. No. 2, 2e-21;
 Matches 47; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 2 TAVALGSPAGGPAELSLRLGEPITVSDGDWMTVLSVSGREYNIPSVYAKV 56
 DB 35 TAVALGSPAGGPAELSLRLGEPITVSDGDWMTVLSVSGREYNIPSVYAKV 89

RESULT 5.

Q9H135 PRELIMINARY; PRT; 197 AA.
 AC Q9H135;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE D9J77B1.1 (Novel protein tyrosine kinase with Src homology domain 2 (SH2) domains) (Fragment).
 GN D9J77B1.1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Lloyd D.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL050318; CAB75365.1; -.
 DR HSSP; P06239; ILKK.
 DR InterPro; IPR000980; SH2.
 DR Pfam; PF00017; SH2; 1.
 DR PRINTS; PR00401; SH2DOMAIN.
 DR PRODOM; PD000093; SH2; 1.
 DR SMART; SM00252; SH2; 1.
 DR PROSITE; PSS0001; SH2; 1.
 KW Kinase.
 FT NON_TER
 SQ SEQUENCE 197 AA; 22124 MW; EF01FE7A85C5C1F1 CRC64;

Query Match

Best Local Similarity 49.7%; Score 143; DB 4; Length 197;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 DGDWTVLSEVSGREYNIPSVHAKV 56
 1 DGDWTVLSEVSGREYNIPSVHAKV 26

RESULT 6

Q96Q14 PRELIMINARY; PRT; 63 AA.
 AC Q96Q14;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE D1460J8.2 (Novel protein tyrosine kinase with Src homology 2 (SH2) domain) (Fragment).
 GN D1460J8.2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Skuce C.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL031662; CAC44645.1; -.
 KW Kinase.
 FT NON_TER
 SQ SEQUENCE 63 AA; 6350 MW; 3EC599C9F1723053 CRC64;

Query Match 48.6%; Score 140; DB 4; Length 63;
 Best Local Similarity 100.0%; Pred. No. 1e-09;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATAVAGSPAGGPAELSLRIGEPITVS 29
 35 ATAVAGSPAGGPAELSLRIGEPITVS 63

RESULT 7

Q77050

ID Q77050 PRELIMINARY; PRT; 517 AA.

AC Q77050;
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Src-type protein tyrosine kinase.
 GN ACSRC1.
 OS Anthracaris crassispina (Sea urchin).
 OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa; Echinoidae; Euechinoidae; Echinacea; Echinoida; Echinometridae; Anthracidaris.
 OX NCBI_TaxId=7629;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Onodera H., Kobari K., Sakuma M., Sato M., Suyemitsu T., Yamasu K.;
 RT "Expression of a src-type protein tyrosine kinase gene, Acsrcl, in the sea urchin embryo.";
 RL Dev. Growth Differ. 0:0-0(1999).
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
 DR EMBL; AB016815; BAA33741.1; -.
 DR HSSP; P00523; 2PTK.
 DR InterPro; IPR000719; Euk_pkinase.
 DR InterPro; IPR000980; SH2.
 DR InterPro; IPR001452; SH3.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR Pfam; PF00069; pkinase; 1.
 DR Pfam; PF00017; SH2; 1.
 DR Pfam; PF00018; SH3; 1.
 DR PRINTS; PR00401; SH2DOMAIN.
 DR PRINTS; PR00452; SH3DOMAIN.
 DR PRINTS; PR00109; TYRKINASE.
 DR PRODOM; PD000001; Euk_pkinase; 1.
 DR PRODOM; PD000066; SH3; 1.
 DR PRODOM; PD000093; SH2; 1.
 DR SMART; SM00252; SH2; 1.
 DR SMART; SM00326; SH3; 1.
 DR SMART; SM00219; TYRK; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00114; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS00001; SH2; 1.
 DR PROSITE; PS00002; SH3; 1.
 KW ATP-binding; Kinase; SH3 domain; Transferase; Tyrosine-protein kinase.
 SQ SEQUENCE 517 AA; 58568 MW; D249A3DC35E83CA1 CRC64;

Query Match

Best Local Similarity 38.0%; Score 109.5; DB 5; Length 517;
 Matches 24; Conservative 11; Mismatches 20; Indels 1; Gaps 1;

QY 2 TAVAGSPAGGPAELSLRIGEPITVS-DGDWTVLSEVSGREYNIPSVHAKV 56
 68 TVALVDYDARSESDLSFKGKGLTILNWDGWLAKSNVTERDGYIPSVIAPV 123

RESULT 8

Q96IN1 PRELIMINARY; PRT; 505 AA.
 AC Q96IN1;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Unknown (protein for MGC:16168).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Straube R.;
 RC Tissue=lymph;
 RA Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC007371; AA07371.1; -.
 DR InterPro; IPR000719; Euk_pkinase.

DR InterPro; IPR000980; SH2.
 DR InterPro; IPR001452; SH3.
 DR Pfam; PF000069; Kinase; 1.
 DR Pfam; PF00017; SH2; 1.
 DR Pfam; PF00018; SH3; 1.
 DR ProDom; PD000001; Euk_kinase; 1.
 DR ProDom; PD000066; SH3; 1.
 DR ProDom; PD000093; SH2; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS50001; SH2; 1.
 DR PROSITE; PS50002; SH3; 1.
 DR ATP-binding; Transferase.
 SO SEQUENCE 505 AA; 57706 MW; B5F739BEF8389176 CRC64;

Query Match 34.7%; Score 100; DB 4; Length 505;
 Best Local Similarity 41.5%; Pred. No. 0.00091;
 Matches 22; Conservative 8; Mismatches 23; Indels 0; Gaps 0;

QY 4 VALGSPAGPAELSLRLGEPPLTVSEDDGWTVLSEVSGREYNIPSYHAKV 56
 DB 64 VALDYTYTAMNDRLQMLKGEKLVKGTGDWTLARSLVYRGEGVPSNFAV 116

RESULT 9

Q9HB17 PRELIMINARY; PRT; 161 AA.

AC Q9HB17; 01-MAR-2001 (TREMblrel. 16, Created)
 DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)
 DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
 DE Src-1-like adapter protein (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 ON NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Blechschmidt K., Kalaydjieva L., Goodman R., Gresham D., Baas F.,
 RA Jonge, Rd., Schilhabel M.B., Menzel U., Detle M.D., Baumgart C.,
 RA Jahn N., Rosenthal A.;
 RT "Chromosome 8 genomic sequence."
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Genome Sequencing Center Jena;
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
 DR EMBL; AF235100; AAC29878.1; -.
 DR HSSP; P08631; 3HCK.
 DR InterPro; IPR000980; SH2.
 DR InterPro; IPR001452; SH3.
 DR Pfam; PF00017; SH2; 1.
 DR Pfam; PF00018; SH3; 1.
 DR PRINTS; PR00401; SH2DOMAIN.
 DR ProDom; PD000093; SH2; 1.
 DR ProDom; PD000252; SH2; 1.
 DR SMART; SM00326; SH3; 1.
 DR SMART; SM00326; SH3; 1.
 DR PROSITE; PS50001; SH2; 1.
 DR PROSITE; PS50002; SH3; 1.
 DR SH3 domain.
 KW SH3 domain.
 FT NON TER
 SO SEQUENCE 161 AA; 18493 MW; FC285466804E5B20 CRC64;

Query Match 34.4%; Score 99; DB 4; Length 161;
 Best Local Similarity 37.3%; Pred. No. 0.0003;
 Matches 19; Conservative 11; Mismatches 21; Indels 0; Gaps 0;

QY 6 LGSFPAAGPAELSLRLGEPPLTVSEDDGWTVLSEVSGREYNIPSYHAKV 56
 DB 30 LSDYSPDISPPIFRGKELRVISDEGGMWKAISLSTGRESYIPGICVAV 80

RESULT 10

Q13239 PRELIMINARY; PRT; 276 AA.

AC Q13239; 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
 DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
 DE Putative SRC-1-like adapter protein (SLAP) (SRC-1-like-adapter).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 ON NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96423054; PubMed=8825655;
 RA Angier M., Wells D.E., Chakravarti A., Pandey A.;
 RT "Chromosomal localization of the mouse Src-1-like adapter protein (Slap) gene and its putative human homolog SLA.";
 RL Genomics 30:623-625(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=BRIN;
 RA Weijerink P.H.S., Zorn G., Bikker H., Bolhuis P.A., Baas F.;
 RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Ohtsuki T., Hatake K., Ikeda M., Tomizuka H., Terui Y., Uwai M.,
 RA Miura Y.;
 RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Blechschmidt K., Kalaydjieva L., Goodman R., Gresham D., Baas F.,
 RA Jonge, Rd., Schilhabel M., Wen G., Menzel U., Detle M., Baumgart C.,
 RA Rosenthal A.;
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 RN [5]

RP SEQUENCE FROM N.A.
 RC TISSUE=BONE MARROW;
 RA Strausberg R.;
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
 DR EMBL; U30473; AAC50357.1; -.
 DR EMBL; U44403; AAC27662.1; -.
 DR EMBL; D89077; BA013758.1; -.
 DR EMBL; AF305872; BA017933.1; -.
 DR EMBL; BC007042; AA07042.1; -.
 DR HSSP; P08631; 3HCK.
 DR InterPro; IPR000980; SH2.
 DR InterPro; IPR001452; SH3.
 DR Pfam; PF00017; SH2; 1.
 DR Pfam; PF00018; SH3; 1.
 DR PRINTS; PR00401; SH2DOMAIN.
 DR ProDom; PD000093; SH2; 1.
 DR ProDom; PD000252; SH2; 1.
 DR SMART; SM00326; SH3; 1.
 DR SMART; SM00326; SH3; 1.
 DR PROSITE; PS50001; SH2; 1.
 DR PROSITE; PS50002; SH3; 1.
 DR SH3 domain.
 KW SH3 domain.
 SO SEQUENCE 276 AA; 31156 MW; B0FC7D7B2ECA378 CRC64;

Query Match 34.4%; Score 99; DB 4; Length 276;
 Best Local Similarity 37.3%; Pred. No. 0.00058;
 Matches 19; Conservative 11; Mismatches 21; Indels 0; Gaps 0;

QY 6 LGSFPAAGPAELSLRLGEPPLTVSEDDGWTVLSEVSGREYNIPSYHAKV 56
 DB 30 LSDYSPDISPPIFRGKELRVISDEGGMWKAISLSTGRESYIPGICVAV 80

RESULT 11
 Q80Z8 PRELIMINARY; PRT; 280 AA.

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AC 0804.8;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Src-like adapter protein SLAP (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ILS, AND ISS.
RX MEDLINE=21363810; PubMed=11471062;
RA Ehringer M.A., Thompson J., Controy O., Xu Y., Yang F., Caniff J.,
RA Beeson M., Gordon L., Bennett B., Johnson T.E., Sikela J.M.;
RT "High-throughput sequence identification of gene coding variants
RT within alcohol-related Orls."
RL Mamm. Genome 12:657-663(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=ILS, AND ISS.
RX Ehringer M.A., Thompson J., Controy O., Xu Y., Yang F., Caniff J.,
RA Beeson M., Gordon L., Bennett B., Johnson T.E., Sikela J.M.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY079449; AL87537.1; -
DR EMBL: AY079450; AL87538.1; -
FT NON_TER 1
FT SEQUENCE 280 AA; 31549 MW; A05C3BF7FED951 CRC64;
SQ
Query Match 33.7%; Score 97; DB 11; Length 280;
Best Local Similarity 37.3%; Pred. No. 0.001;
Matches 19; Conservative 11; Mismatches 21; Indels 0; Gaps 0;

Qy 6 LGSFPAAGPAELSLRLGPELTIVSESGDWMVTVLSEVSGREYNIPSHVAVY 56
Db 29 LDYSPDISPPIFRGEXKLRIIVSDGGMWKALSLSTGRESYIPGICVAVY 79

RESULT 12
ID 060898 PRELIMINARY; PRT; 281 AA.
AC 060898;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE SRC-like adapter protein.
GN SLA OR SLAP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95370243; PubMed=7543898;
RA Pandey A., Duan H., Dixit V.M.;
RT "Characterization of a novel Src-like adapter protein that associates
RT with the Etk receptor tyrosine kinase."
RL J. Biol. Chem. 270:19201-19204(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20093985; PubMed=10630289;
RA Carrier A., Nguyen C., Vactorero G., Granjeaud S., Rocha D.,
RA Bernard K., Miazek A., Ferrier P., Malissen M., Naquet P.,
RA Malissen B., Jordan B.;
RT "Differential gene expression in CD3e- and RAG1-deficient thymuses:
RT definition of a set of genes potentially involved in thymocyte
RT maturation."
RL Immunogenetics 50:255-270(1999).
CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
DR EMBL: U29056; AAA82756.1; -
DR EMBL: AJ131777; CAB6139.1; -
DR HSSP: P16277; IBLK.

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DR MCD; MCI:104295; SLA.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR001452; SH3.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF00018; SH3; 1.
DR PRINTS; PR00401; SH2DOMAIN.
DR ProDom; PD000093; SH2; 1.
DR SMART; SM00252; SH2; 1.
DR SMART; SM00326; SH3; 1.
DR PROSITE; PS50001; SH2; 1.
DR PROSITE; PS50002; SH3; 1.
DR KX SH3 domain.
SQ SEQUENCE 281 AA; 31680 MW; B347921656A7ADA1 CRC64;

Query Match 33.7%; Score 97; DB 11; Length 281;
Best Local Similarity 37.3%; Pred. No. 0.001;
Matches 19; Conservative 11; Mismatches 21; Indels 0; Gaps 0;

Qy 6 LGSFPAAGPAELSLRLGPELTIVSESGDWMVTVLSEVSGREYNIPSHVAVY 56
Db 30 LDYSPDISPPIFRGEXKLRIIVSDGGMWKALSLSTGRESYIPGICVAVY 80

RESULT 13
ID 09Y121 PRELIMINARY; PRT; 527 AA.
AC 09Y121;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Protein tyrosine kinase.
GN EPPK3 OR EPPK2.
OS Ephydaria fluvitilis.
OC Eukaryota; Metazoa; Porifera; Demospongiae; Ceraclimorpha;
OC Haploecetida; Spongillidae; Ephydaria.
OX NCBI_TaxId=31330;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99246375; PubMed=10229568;
RA Suga H., Koyanagi M., Hoshiyama D., Ono K., Iwabe N., Kuma K.,
RA Miyata T.;
RT "Extensive gene duplication in the early evolution of animals before
RT the parazoan-eumetazoan split demonstrated by G proteins and protein
RT tyrosine kinases from sponge and hydra."
RL J. Mol. Evol. 48:646-653(1999).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21601119; PubMed=11738833;
RA Suga H., Katoh K., Miyata T.;
RT "Sponge homologs of vertebrate protein tyrosine kinases and frequent
RT domain shufflings in the early evolution of animals before the
RT parazoan-eumetazoan split."
RL Gene 280:195-201(2001).
DR EMBL; AB006557; BAA81711.2; -
DR EMBL; AB049592; BAB82421.1; -
DR HSSP; P11362; IFCK.
DR InterPro; IPR000719; Euk_Pkinase.
DR InterPro; IPR002280; Set_thr_Pkinase.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR001452; SH3.
DR InterPro; IPR001245; Tyr_Pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF00018; SH3; 1.
DR PRINTS; PR00401; SH2DOMAIN.
DR PRINTS; PR00452; SH3DOMAIN.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000066; SH3; 1.
DR ProDom; PD000093; SH2; 1.
DR SMART; SM00252; SH2; 1.
DR SMART; SM00326; SH3; 1.
DR SMART; SM00220; S_TKc; 1.

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DR SMART; SM00219; TykC; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS50001; SH2; 1.
 DR PROSITE; PS50002; SH3; 1.
 KW Kinase
 SO SEQUENCE 527 AA; 58101 MW; FE1E1EA836DF5C39 CRC64;

Query Match 33.2%; Score 95.5; DB 5; Length 527;
 Best Local Similarity 42.6%; Pred. No. 0.0034;
 Matches 23; Conservative 9; Mismatches 21; Indels 1; Gaps 1;

QY 2 TVALGSPAGPAELSLRLGPTLVSESGRENYIPSVYAKV 54
 DB 79 TFLVLYKRDRTKEDLSEFKGBNLIITIKODGWWLARSLTGKGYIPSNYA 132

RESULT 14
 ID Q9V9J3 PRELIMINARY; PRT; 517 AA.
 AC Q9V9J3. 01-MAR-2002 (Tremblrel. 20, Created)
 DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
 DE Src-family protein tyrosine kinase.
 OS Strongylocentrotus purpuratus (Purple sea urchin).
 OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
 OC Strongylocentrotidae; Echinoidea; Echinacea; Echinoida; Strongylocentrotidae;
 OC Strongylocentrotus.
 NX NCBI_TaxID=7668;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Giusti A.F., O'Neill F.J., Yamao K., Foltz K.R., Jaffe L.A.;
 RT "Function of a sea urchin egg src-family kinase in initiating Ca2+
 RT release at fertilization."
 RT Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AY063749; AML5011.1; -
 DR InterPro; IPR0000719; Euk_pkinase.
 DR InterPro; IPR002280; Set_tmr_pkinase.
 DR InterPro; IPR000980; SH2.
 DR InterPro; IPR001452; SH3.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR Pfam; PF00069; pkinase; 1.
 DR Pfam; PF00017; SH2; 1.
 DR Pfam; PF00018; SH3; 1.
 DR PRINTS; PR00401; SH2DOMAIN.
 DR PRINTS; PR00452; SH3DOMAIN.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Euk_pkinase; 1.
 DR ProDom; PD000066; SH3; 1.
 DR ProDom; PD000093; SH2; 1.
 DR SMART; SM00252; SH2; 1.
 DR SMART; SM00326; SH3; 1.
 DR SMART; SM00220; S_TKC; 1.
 DR SMART; SM00219; TykC; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; UNKNOWN; 1.
 DR PROSITE; PS50001; SH2; 1.
 DR PROSITE; PS50002; SH3; 1.
 KW Kinase.
 SO SEQUENCE 511 AA; 57726 MW; D3856B7B0D46716D CRC64;

Query Match 32.3%; Score 93; DB 5; Length 511;
 Best Local Similarity 36.5%; Pred. No. 0.0065;
 Matches 19; Conservative 10; Mismatches 23; Indels 0; Gaps 0;

QY 5 ALGSPAGPAELSLRLGPTLVSESGRENYIPSVYAKV 56
 DB 67 ALYDARSDDDDPKKGIILVVTBDDWMLARSKTKGKYIPSNYAPV 118

RESULT 15
 ID Q9V9J3 PRELIMINARY; PRT; 517 AA.
 AC Q9V9J3. 094879; Q18369; Q26297;
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
 DE Tyrosine-protein kinase Src42A (EC 2.7.1.112).
 GN SRC42A OR SRC41 OR TK5 OR CG7873.
 OS Drosophila melanogaster (fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 NX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A., FUNCTION, TISSUE SPECIFICITY, AND DEVELOPMENTAL
 RP STAGE.
 RP STRAIN=CANTON-S; TISSUE=PUPAE;
 RX MEDLINE=96268448; PubMed=8682295;
 RA Takahashi F., Endo S., Kojima T., Saigo K.;
 RT "Regulation of cell-cell contacts in developing Drosophila eyes by
 RT Dsrc4, a new, close relative of vertebrate c-src."
 RL Genes Dev. 10:1645-1656(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RP STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Abell J.F., Agbayani A., An H.-J., Andrews-Frankoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu U., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhattacharya D., Bolshakov S.,
 RA Botkova D., Botchan M.R., Bouck J., Brooksstein P., Brottier P.,
 RA Buttle J.K., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.C., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA De Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Dudin K.J., Evangelista C.C., Ferrar C., Ferrera S., Fleischmann W.,
 RA Folsler C., Gabrielian A.E., Garg N.S., Gelbart M.M., Glasel K.,
 RA Glöckner A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris B.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hootin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jaitani M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kuip D., Lai Z.,
 RA Laoko P., lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattaei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Mleishina N.V., Modarity C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy L., Murthy D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacle J.M.,
 RA Palazzotto M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun B.,
 RA Svrtk R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster."
 RL Science 287:2185-2195(2000).
 RN [3]
 RP SEQUENCE FROM N.A.
 RP STRAIN=BERKELEY; TISSUE=EMBRYO;
 RC Stapleton M., Brooksstein P., Hong L., Agbayani A., Carlson J.,
 RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
 RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
 RA Nuno J., Pacle J., Paragas V., Park S., Phouanavong S., Wan K.,
 RA Yu C., Lewis S.E., Rubin G.M., Celinker S.;

RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 RN [1]
 RP SEQUENCE OF 374-428 FROM N.A.
 RX MEDLINE=9200631; PubMed=1915852;
 RA Shihido E., Emori Y., Saigo K.;
 RT "Identification of seven novel protein-tyrosine kinase genes of
 RL Drosophila by the polymerase chain reaction.";
 RN FEBS Lett. 289:235-238 (1991).
 RP SEQUENCE OF 376-427 FROM N.A.
 RC TISSUE=EMBRYO;
 RX MEDLINE=98401146; PubMed=9711193;
 RA Oates A.C., Wolberg P., Achen M.G., Wilks A.F.;
 RT "Sampling the genomic pool of protein tyrosine kinase genes using the
 RT polymerase chain reaction with genomic DNA."
 RL Biochem. Biophys. Res. Commun. 249:660-667 (1998).
 CC -1- FUNCTION: ESSENTIAL FOR CORRECT EYE MORPHOGENESIS (OMMATIDIAL R7
 CC NEURON FORMATION), THIS REQUIRES THE RAS1/MAPK SIGNAL TRANSDUCTION
 CC ORGANIZATION AND CELL-CELL CONTACTS IN DEVELOPING OMMATIDIA.
 CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP + PROTEIN
 CC TYROSINE PHOSPHATE.
 CC -1- TISSUE SPECIFICITY: UBIQUITOUS IN EARLY EMBRYOS, IN STAGES 13-16
 CC EXPRESSION IS SEEN IN VISCERAL MESODERM, HINDGUT, BRAIN, ANAL PADS
 CC AND VENTRAL GANGLIONS. IN LARVAE, EXPRESSION IS IN CNS, WING DISK,
 CC POSTERIOR TO THE MORPHOGENETIC FURROW.
 CC -1- DEVELOPMENTAL STAGE: IN EARLY EMBRYOS EXPRESSION IS VERY LOW,
 CC EXPRESSION INCREASES DURING EMBRYOGENESIS. ALSO EXPRESSED IN
 CC LARVAE AND PUPAE.
 CC -1- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
 CC DOMAIN. BELONGS TO THE SRC SUBFAMILY.
 CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
 DR EMBL; D42325; BAA07705.1; -;
 DR EMBL; AE003784; AAF57295.1; -;
 DR EMBL; AY058652; AAL13881.1; -;
 DR EMBL; S55977; AAB19907.1; -;
 DR EMBL; AJ002911; CAA05746.1; -;
 DR HSSP; P00523; ISRL.
 DR FlyBase; FBgn004603; Src42A.
 DR InterPro; IPR000719; Euk_pkinase.
 DR InterPro; IPR000980; SH2.
 DR InterPro; IPR001452; SH3.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR Pfam; PF00069; pkinase; 1.
 DR Pfam; PF00017; SH2; 1.
 DR Pfam; PF00018; SH3; 1.
 DR PRINTS; PRO0401; SH2DOMAIN.
 DR PRINTS; PRO0452; SH3DOMAIN.
 DR PRINTS; PRO0109; TYRKINASE.
 DR ProDom; PD000001; Euk_pkinase; 1.
 DR ProDom; PD000066; SH3; 1.
 DR ProDom; PD000093; SH2; 1.
 DR SMART; SM00252; SH2; 1.
 DR SMART; SM00326; SH3; 1.
 DR SMART; SM00219; TYKC; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TIR; 1.
 DR PROSITE; PS50001; SH2; 1.
 DR PROSITE; PS50002; SH3; 1.
 KW transferase; kinase; tyrosine-protein kinase; ATP-binding; SH2 domain;
 KW SH3 domain; developmental protein.
 FT DOMAIN 63 124 SH3.
 FT DOMAIN 130 222 SH2.
 FT DOMAIN 248 504 PROTEIN_KINASE.
 FT NP_BIND 254 252 ATP (BY SIMILARITY).
 FT BINDING 276 276 ATP (BY SIMILARITY).
 FT ACT_SITE 370 370 BY SIMILARITY.
 FT CONFLICT 65 65 A -> V (IN REF. 1).
 FT CONFLICT 376 376 V -> I (IN REF. 4 AND 5).
 FT CONFLICT 381 386 GNIVKI -> SNVVKM (IN REF. 4).

SO SEQUENCE 517 AA; 59069 MW; 1EF196E4D7AE61B9 CRC64;
 Query Match 31.8%; Score 91.5; DB 5; Length 517;
 Best Local Similarity 42.6%; Pred. No. 0.01;
 Matches 23; Conservative 9; Mismatches 21; Indels 1; Gaps 1;
 Oy 4 VALGSPAGGPAELSLRLGEPITVSE-DGDMWTVLSEVSGREYNIPSVHAKV 56
 Db 69 VALVDYDARTDEDLSFRKGEHLLEINDQDWWLARSKTRSEGYIPSNVAVL 122
 Search completed: March 24, 2003, 15:50:35
 Job time : 10.4182 secs

